NCBI   ☉Nucleotide

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ Go | Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ | Save | Text | Add to Clipboard

⌐1: D45218. Rice mRNA for pho...[gi:639685]   Related Sequences, Protein, PubMed, Taxonomy, LinkOut

```
LOCUS       RICPGIB                 2009 bp    mRNA    linear   PLN 10-FEB-1999
DEFINITION  Rice mRNA for phosphoglucose isomerase (Pgi-b), complete cds.
ACCESSION   D45218
VERSION     D45218.1  GI:639685
KEYWORDS    phosphoglucose isomerase; Pgi-b.
SOURCE      Oryza sativa cDNA to mRNA.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 2009)
  AUTHORS   Uchimiya,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1995) Hirofumi Uchimiya, Institute of Mol. &
            Cell. Bioscience, The Unversity of Tokyo, Department of Cellular
            Function; 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan
            (E-mail:huchimiy@tansei.cc.u-tokyo.ac.j p,
            Tel:03-3812-2111(ex.7844), Fax:03-3812-2910)
REFERENCE   2  (bases 1 to 2009)
  AUTHORS   Nozue,F., Umeda,M., Nagamura,Y., Minobe,Y. and Uchimiya,H.
  TITLE     Characterization of cDNA encoding for phosphoglucose isomerase of
            rice (Oryza sativa L.)
  JOURNAL   DNA Seq. 6 (3), 127-135 (1996)
  MEDLINE   96293857
   PUBMED   8722567
FEATURES             Location/Qualifiers
     source          1..2009
                     /organism="Oryza sativa"
                     /db_xref="taxon:4530"
     CDS             54..1760
                     /codon_start=1
                     /product="phosphoglucose isomerase (Pgi-b)"
                     /protein_id="BAA08149.1"
                     /db_xref="GI:639686"
                     /translation="MASSALICDTEQWKGLQAHVGAIQKTHLRDLMDDAERCKAMTAE
                     YEGIFLDYSRQRATGETMEKLFKLAEAAKLKEKIEKMFSGDKINSTENRSVLHVALRA
                     PRDEVIKSDGVNVVPEVWGVKDKIKQFSETFRSGSWVGATGKALTNVVSVGIGGSFLG
                     PLFVHAALQTDPEAAESAKGRQLRFLANVDPVDVARSIKDLDPETTLVVVVSKTFTTA
                     ETMLNARTLQWSGLSLLLGPDAVAKHMIAVSTNLELVEKFGIDPKNAFAFWDWVGGRY
                     SVCSAVGVLPLSLQYGFPIVQKFLEGAASIDKHFRSSSFEKNIPVLLGLLSVWNVSFL
                     GYPARAILPYSQALEKFAPHIQQLSMESNGKGVSIDGVQLPFESGEIDFGEPGTNGQH
                     SFYQLIHQGRVIPCDFIGVVKSQQPVYLKGEIVSNHDELMSNFFAQPDALAYGKTPEQ
                     LHSEKVPEHLISHKTFQGNRPSLSLLLPSLSAYEIGQLLSIYEHRIAVQGFLWGINSF
                     DQWGVELGKSLASQVRKSLHASRMEGKPVQGFNSSTASLLTRYLAVEPSTPYNTTTMP
                     KV"
     polyA_site      2009
BASE COUNT      539 a    412 c    485 g    573 t
ORIGIN
        1 gatccgcttc ctcatccacc gatcgccccc tccttcatcc tccggtagca gtcatggcgt
       61 cgtcggcgct aatctgcgac accgagcagt ggaagggcct ccaggcgcac gtcggggcga
      121 ttcagaagac gcacctgcgc gatctgatgg atgatgccga cgcgctgcaag gcaatgacag
      181 ctgagtatga aggcatattt ctggattact cgaggcagcg tgcaactggc gagaccatgg
```
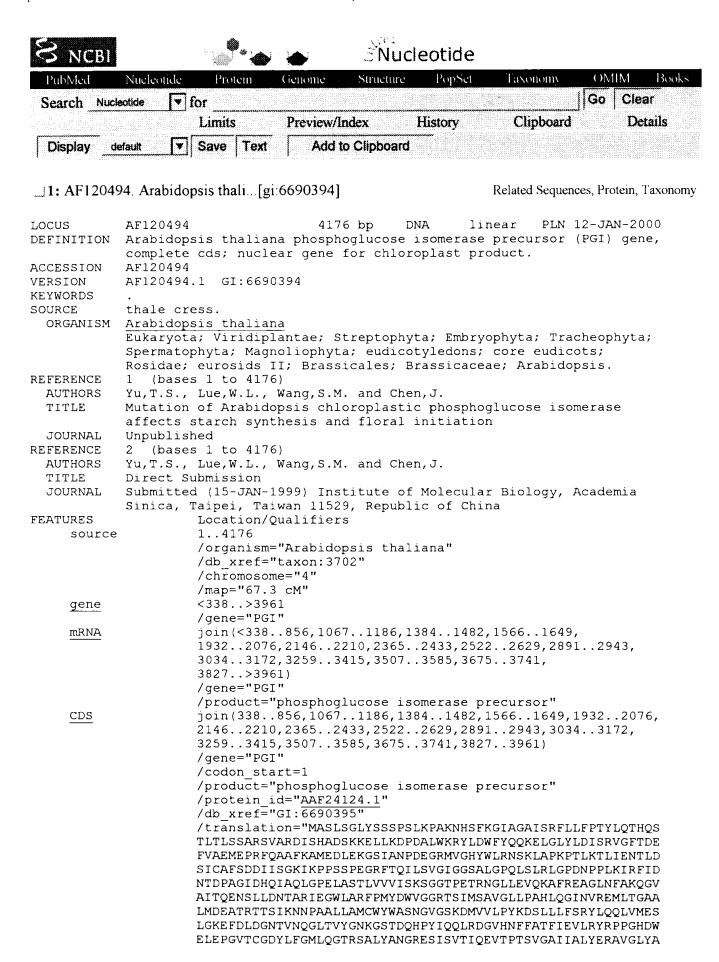
```
 241 agaagctgtt taaattggca gaggcggcaa agctcaagga gaagattgag aagatgttta
 301 gtggtgacaa gataaatagc acagagaaca gatctgtgct tcatgtagct ctaagggctc
 361 caagagacga agtaataaaa agtgatgggg tcaatgtggt tcccgaagtt tggggtgtaa
 421 aagataaaat caagcagttt tcagaaactt ttaggagtgg atcatgggtt ggggcaactg
 481 gtaaagcatt gacaaatgtt gtgtcagttg gaataggtgg tagctttctt ggtcctctgt
 541 tcgtgcatgc tgccctccag acagatccag aagctgcaga atctgccaaa gggcgacagt
 601 taagattcct tgcaaatgtt gaccctgttg atgttgcacg aagcatcaaa gatttagatc
 661 ctgaaacaac acttgttgtg gttgtctcaa agaccttcac aacagctgaa acaatgttaa
 721 atgctcgaac tctacaatgg agtggattgt ctcttctgct tggacctgat gctgttgcga
 781 aacatatgat tgctgtcagt accaatcttg agcttgtgga gaagtttgga attgaccota
 841 aaaatgcttt tgcattttgg gactgggttg gtggtcgcta tagtgtttgc agtgctgttg
 901 gtgtcctgcc cttatctctt caatatggtt ttccgattgt tcagaaattt ttggagggtg
 961 cagccagcat cgacaaacac ttccgttcat cttcatttga gaaaaacata cctgtactcc
1021 ttggtttgct gagtgtgtgg aatgtttcct ttcttggata tccagctaga gcaatactgc
1081 cctattccca agcacttgag aaatttgcac cgcatattca gcagcttagc atggagagta
1141 atggaaaggg tgtctccatt gatggtgttc aactgccctt tgagagtggt gaaattgatt
1201 ttggtgaacc tggaaccaat gggcaacaca gcttctatca attaatccat cagggaagag
1261 ttattccttg tgattttatc ggcgtcgtga aaagccagca acccgtttac ttgaaagggg
1321 aaattgtgag caatcatgac gaattgatgt ccaatttctt tgctcagcct gatgcacttg
1381 cttatggaaa gacccctgaa caactgcaca gcgagaaagt acctgaacat cttatctctc
1441 ataagacttt tcagggcaac cgaccatcac ttagtttatt gctgccctca ttatctgctt
1501 atgagattgg acagctttta tccatctacg agcaccggat tgcagttcag ggtttcctat
1561 ggggaataaa ctcatttgac cagtggggag tggaactggg aaagtctctg gcttctcaag
1621 tgagaaaatc tctgcatgca tcccgcatgg aaggaaagcc tgtccagggg ttcaacagca
1681 gcactgcaag tttgctgaca cgatatctcg ctgttgagcc atccactcct tacaacacta
1741 caacaatgcc gaaagtttaa tatgatgtgt ttggcacgct attttctttg agttaaacaa
1801 ggttgagccg gcatattctg taataagttt atttatgttc cttttgaagt tgttacaggc
1861 ttacagcccg ttttacagta ccatagtttt gttgtttttt tcttttattt tactccgact
1921 tccaggagaa caaaatggaa aagaaaaagg aaaggaaact attttgcaat aaataaatta
1981 attcgtgtca gcatgaggaa actatcact
```
//

Revised: October 24, 2001.

May 24 2002 12:14:27

NCBI

Nucleotide

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ Go | Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save | Text | Add to Clipboard

1: AF120494. Arabidopsis thali...[gi:6690394]   Related Sequences, Protein, Taxonomy

```
LOCUS       AF120494                4176 bp    DNA     linear   PLN 12-JAN-2000
DEFINITION  Arabidopsis thaliana phosphoglucose isomerase precursor (PGI) gene,
            complete cds; nuclear gene for chloroplast product.
ACCESSION   AF120494
VERSION     AF120494.1  GI:6690394
KEYWORDS    .
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 4176)
  AUTHORS   Yu,T.S., Lue,W.L., Wang,S.M. and Chen,J.
  TITLE     Mutation of Arabidopsis chloroplastic phosphoglucose isomerase
            affects starch synthesis and floral initiation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4176)
  AUTHORS   Yu,T.S., Lue,W.L., Wang,S.M. and Chen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1999) Institute of Molecular Biology, Academia
            Sinica, Taipei, Taiwan 11529, Republic of China
FEATURES             Location/Qualifiers
     source          1..4176
                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
                     /chromosome="4"
                     /map="67.3 cM"
     gene            <338..>3961
                     /gene="PGI"
     mRNA            join(<338..856,1067..1186,1384..1482,1566..1649,
                     1932..2076,2146..2210,2365..2433,2522..2629,2891..2943,
                     3034..3172,3259..3415,3507..3585,3675..3741,
                     3827..>3961)
                     /gene="PGI"
                     /product="phosphoglucose isomerase precursor"
     CDS             join(338..856,1067..1186,1384..1482,1566..1649,1932..2076,
                     2146..2210,2365..2433,2522..2629,2891..2943,3034..3172,
                     3259..3415,3507..3585,3675..3741,3827..3961)
                     /gene="PGI"
                     /codon_start=1
                     /product="phosphoglucose isomerase precursor"
                     /protein_id="AAF24124.1"
                     /db_xref="GI:6690395"
                     /translation="MASLSGLYSSSPSLKPAKNHSFKGIAGAISRFLLFPTYLQTHQS
                     TLTLSSARSVARDISHADSKKELKDPDALWKRYLDWFYQQKELGLYLDISRVGFTDE
                     FVAEMEPRFQAAFKAMEDLEKGSIANPDEGRMVGHYWLRNSKLAPKPTLKTLIENTLD
                     SICAFSDDIISGKIKPPSSPEGRFTQILSVGIGGSALGPQLSRLGPDNPPLKIRFID
                     NTDPAGIDHQIAQLGPELASTLVVVISKSGGTPETRNGLLEVQKAFREAGLNFAKQGV
                     AITQENSLLDNTARIEGWLARFPMYDWVGGRTSIMSAVGLLPAHLQGINVREMLTGAA
                     LMDEATRTTSIKNNPAALLAMCWYWASNGVGSKDMVVLPYKDSLLLFSRYLQQLVMES
                     LGKEFDLDGNTVNQGLTVYGNKGSTDQHPYIQQLRDGVHNFFATFIEVLRYRPPGHDW
                     ELEPGVTCGDYLFGMLQGTRSALYANGRESISVTIQEVTPTSVGAIIALYERAVGLYA
```

```
                         SIVNINAYHQPGVEAGKKAAAEVLALQKRVLSVLNEATCKDPVEPLTLEEIADRCHAP
                         EEIEMIYKIIAHMSANDRVLIAEGNCGSPRSIKVYLGECNVDDLYA"
         transit_peptide 338..556
                         /gene="PGI"
         polyA_site      4109
         polyA_site      4176
BASE COUNT      1153 a      829 c      859 g     1335 t
ORIGIN
        1 aaaagagtgg tagttattct gaatagaaag aaacatctgg aaatggcggg cacgtgaata
       61 aaatagaata tgatgccaat tgagacaata atatatatac atagtcgtaa taagagtgat
      121 aaaagctttg tgaagactac ctaatctaag ctcccaccaa aggacaaatc tctctcccgc
      181 actcatctct gttcattggt tcctcccaaa aaatatcaat caaatcggaa taaactatac
      241 gaatcctcca atataaagct ccaccctttc tctttctatc tctctctctc cattgttgac
      301 tgtctctctt ccctcgtaaa catcgctgtc tctaaagatg gcctctctct caggcctata
      361 ctcttcttct ccatctctca aacctgccaa aaaccattct tttaaaggca ttgccggcgc
      421 aatctcgaga ttccttctct ttcccacata cctccaaacc caccaatcta cgttgactct
      481 ctcctcggct cgttctgtgg cacgcgacat ttctcatgcg gattcgaaga aagagcttct
      541 taaggatccg gatgcgttgt ggaagcgata cctcgattgg ttttatcagc agaaagagct
      601 tgggttgtat ctggatatta gtcgggtcgg atttaccgat gagtttgtgg ctgaaatgga
      661 gccaaggttt caagctgcgt ttaaggctat ggaggatctt gaaaaagggt ctatagcgaa
      721 tcctgatgaa ggaagaatgg ttggacatta ctggcttagg aactctaagc tcgcacctaa
      781 gcctacttta aagaccttga tcgagaacac acttgattct atttgcgctt ctccgacga
      841 cataatctct ggaaaggtca gtttttgatc ccaccggcct tgtttggcat tatgatcgta
      901 atggaaaaga tagtttttatg cagagtgtct tacttagatc accttttgag tgttgtttgg
      961 aaatttctga tgctggaaag atagttgtat gcagagtctt acttagctca ccttttttgaa
     1021 tcttgtttgt ttgttactcc cactcaattt tgtttgtatg ttgcagataa agccaccatc
     1081 ttctcctgag ggtcgtttta ctcagatact ttctgttggc attggaggct cggctcttgg
     1141 acctcaattg tcgctgaggc ttggtcctga taatcctcca ttgaaggtat cgcatacgtt
     1201 ctaattgcag tcaacattac attcccttgc tcttaacact cttagccatc cccactaaca
     1261 aatgggtgtt ctttatcttt gcctcgtaaa aggatgtcct ctcttaggtt tttctgatta
     1321 aaagagtcta ccttttgttgt ctactgtttt ctgactttat gttcttcctt tggttgttga
     1381 cagataagat tcattgacaa caccgaccct gctggaattg atcatcagat tgcacaactt
     1441 gggccagagc tggcttcgac tttagtagtt gtcatctcaa aggtgtgtcc tatattcagt
     1501 tgtgtttata tgatggttgg tcctgatatt ggcgagcatg attaagtttc ttacgtattt
     1561 cccagagtgg aggtactcct gaaactagaa atggactact ggaagtgcag aaagcattcc
     1621 gtgaagctgg tctgaatttc gcaaaacagg tgttaatctc aggttttttgt ttccgctttt
     1681 tgctgaaatc catgtctcta cgaacatggg aagaatgctg tatgataatg gtcaaactgg
     1741 tttacacggt tggaaataat ctgagaaaag tggactaatt tttcatctca ttaacaacaa
     1801 caaaaaaaaa aaactggctc tcatggatca ttagacagta gacaccttca gatgtattgg
     1861 atataattta gcttcaactt ctgccccact gtagttcctc agcagcaatt tcgcgctgta
     1921 tgcttatgca gggtgttgca ataacccaag agaactcatt actggataat acggcaagaa
     1981 ttgaaggttg gctagctaga tttcctatgt acgactgggt gggtggaaga acatcaataa
     2041 tgtctgcagt tggtctgctt ccagcgcacc tacagggtaa ttgtacataa gcgtaaactt
     2101 tctatgacca tctttgtatt tacacgaaag catgtcatca tatagggatt aatgttaggg
     2161 agatgcttac tggtgctgct ttaatggatg aggctactag gacaacttcg gtaagtagta
     2221 cttattgcag cttgtgttga agatgagttt acttaccagg ttttagtaga atgtcatatc
     2281 atacggttgg gtttcctgac tcatacactt tagatagtct ctaccatgac tcactctagc
     2341 ctgtaaattt gtttgttgtt tcagatcaag aataaccctg cagcgctctt agctatgtgt
     2401 tggtactggg cttccaatgg cgttggttcc aaggtgtttt tcctcaactt ttttgagagt
     2461 tctaaggcta tcaaggagat tgagttctta ttgaccttat accatcttgc tttctttaca
     2521 ggatatggtt gtccttcctt acaaggatag cttattgcta tttagtcggt atctgcagca
     2581 gctggtcatg gaatcactag gaaaggagtt tgatcttgac ggtaacactg taagcatact
     2641 cttcaatttt ctctgcagta ccccaaatca aagttcatga gcatttactg agaactgaga
     2701 aggtgtaaat tggtcttgca attaatgccc actcttataa atcagaagac cttggttact
     2761 taattacttg tgcacatgat tgagttcagt ttgttaccac tccttcatgg aagaattgaa
     2821 acttgtgtac tgtttcctcg accctgttat tacgagtgtg atcccaagga ccggttcttt
     2881 gaatttgcag gttaatcaag ggttaactgt gtatggaaat aagggaagca cagatcagca
     2941 cccgtgagtt tcatttattc atatagtttt actattgaga gagcatagca ataaggagc
     3001 ttttaacagt atttaatttg tttatttcat tagctacatt caacagctga gagatggtgt
     3061 gcacaatttc tttgcaacct tcatagaagt gttacggtac agaccccctg gtcacgattg
     3121 ggagcttgag ccaggtgtca cttgtggaga ctatctcttt gggatgctac aggtctgatt
     3181 tatgaatctc gtttcgcaca aattagtcag agataatata cactctttag taacactata
     3241 tatggtgaat ttgtccaggg aactagatct gctttatatg caaacggtag agaatccatc
     3301 agtgttacaa tccaggaagt gacaccaaca tctgttgggg ctattatagc tctttatgaa
     3361 agagctgttg gtttatatgc ctcaattgtg aacataaatg cttaccacca acccggtaga
```
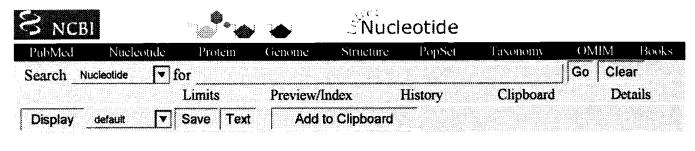
```
3421 gatattcctc ccatatctag aaaccgatgt tctgtaattg cctaattgat atttgtttac
3481 tgaatctgaa taaaaaacga tttcaggtgt ggaagctggg aaaaaggcag cagcagaagt
3541 tctcgccctg caaaagcggg tattgtcagt tcttaatgaa gccacgtaag aatcagaccg
3601 agtccgcttc tttgtcaaaa aatcttgtct cgactcatga gagaccactt atatacttct
3661 ttctgtggct gcagttgtaa agatccggta gagccattga cactggaaga gatagctgat
3721 cgttgtcatg ctcctgagga agtaacgtcc aaatccttga aattgttttt tcattggtaa
3781 cttttcgaac gcacgtatca agaagttttt atctttgaat atgcagatag aaatgatata
3841 caagatcata gcgcacatgt ctgcaaacga cagagttctg atagcagaag gaaactgtgg
3901 atcgccacga agtatcaaag tgtatttggg cgagtgcaat gtggatgacc tgtacgcata
3961 acaaaaccca acactttctc aaactccaaa ctctcattct ctccattcct tatttctttc
4021 tgccatgtct atgattttga aaaagaaaaa gattgcaata agagccagga aacacttgtg
4081 tacttgtttt gaaataaaga taatttcaga atgttacaaa tgttgattgt aatgataaca
4141 ttggagatag attcatcaat caagcaggct catgtg
```
//

Revised: October 24, 2001.

May 24 2002 12:14:27

06/17/02 9:08 AM

NCBI

Nucleotide

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ Go | Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save | Text | Add to Clipboard

1: D45217. Rice mRNA for pho...[gi:639683]   Related Sequences, Protein, PubMed, Taxonomy, LinkOut

```
LOCUS       RICPGIA                 2115 bp    mRNA    linear   PLN 10-FEB-1999
DEFINITION  Rice mRNA for phosphoglucose isomerase (Pgi-a), complete cds.
ACCESSION   D45217
VERSION     D45217.1  GI:639683
KEYWORDS    phosphoglucose isomerase; Pgi-a.
SOURCE      Oryza sativa cDNA to mRNA.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 2115)
  AUTHORS   Uchimiya,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1995) Hirofumi Uchimiya, Institute of Mol. &
            Cell. Bioscience, The Unversity of Tokyo, Department of Cellular
            Function; 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan
            (E-mail:huchimiy@tansei.cc.u-tokyo.ac.j p,
            Tel:03-3812-2111(ex.7844), Fax:03-3812-2910)
REFERENCE   2  (bases 1 to 2115)
  AUTHORS   Nozue,F., Umeda,M., Nagamura,Y., Minobe,Y. and Uchimiya,H.
  TITLE     Characterization of cDNA encoding for phosphoglucose isomerase of
            rice (Oryza sativa L.)
  JOURNAL   DNA Seq. 6 (3), 127-135 (1996)
  MEDLINE   96293857
   PUBMED   8722567
FEATURES             Location/Qualifiers
     source          1..2115
                     /organism="Oryza sativa"
                     /db_xref="taxon:4530"
     CDS             65..1768
                     /codon_start=1
                     /product="phosphoglucose isomerase (Pgi-a)"
                     /protein_id="BAA08148.1"
                     /db_xref="GI:639684"
                     /translation="MASSALICDTEQWKGLQAHVGEIQKTHLRHLMHDVERCKAMTAE
                     YEGIYLDYSRQRATGETMEKLFKLAEAAKLKEKIEKMFRGDKINSTENRSVLHVALRA
                     PRDEVINSNGVNVVPEVWGVKDKIKQFSETFRSGSWVGATGKALTNVVSVGIGGSFLG
                     PLFVHAALQTDPEAAESAKGRQLRFLANVDPVDVARSIKDLDPETTLVVVVSKTFTTA
                     ETMLNARTLKEWIVSSLGPDAVAKHMIAVSTNLELVEKFGIDPKNAFAFWDWVGGRYS
                     VCSAVGVLPLSLQYGFPIVQKFLEGAASIDKHFRSSSFEKNIPVLLGLLSVWNVSFLG
                     YPARAILPYSQALEKFAPHIQQLSMESNGKGVSIDGVQLSFETGEIDFGEPGTNGQHS
                     FYQLIHQGRVIPCDFIGVVKSQQPVYLKGEIVSNHDELMSNFFAQPDALAYGKTPEQL
                     HSEKVPEHLIPHKTFQGNRPSLSLLLPSLSAYEIGQLLAIYEHRIAVQGFLWGINSFD
                     QWGVELGKSLASQVRKSLHASRVEGKPVLGFNSSTTSLLTRYLAVEPSTPYNTTTLPK
                     V"
     polyA_site      2115
BASE COUNT      580 a    424 c    510 g    601 t
ORIGIN
        1 ggaagcgaag cgcggatccg cttcctcacc caccgatcgg cttcttcccc ccacgctagc
       61 agccatggcg tcgtcggcgc tcatctgcga caccgagcag tggaagggcc tccaggcgca
      121 tgttggggag attcagaaaa cgcacctgcg ccatctgatg catgatgttg agcgctgcaa
      181 ggcaatgaca gctgagtatg aaggcatata tctggattac tcgaggcagc gtgcgactgg
```

```
 241 cgaaaccatg gagaagctgt ttaaattggc cgaggctgca aagctcaagg agaagattga
 301 gaagatgttt agaggtgaca agataaatag cacagagaac agatcagtgc ttcatgtagc
 361 tctaagggct ccaagagacg aagtaataaa tagcaatggg gtcaatgtgg ttcccgaagt
 421 ttggggtgta aaagataaaa tcaagcaatt ttcagaaact tttaggagtg gatcatgggt
 481 tggggcaact ggtaaagcat tgacaaatgt tgtgtcagta ggaataggtg gtagctttct
 541 tggtcctctg tttgtgcatg ctgccctcca gacagatcca gaagctgcag aatctgccaa
 601 agggcggcaa ttaagatttc ttgcaaatgt cgaccctgtt gatgttgcac gaagcatcaa
 661 agatttagat cctgaaacaa cacttgttgt ggtagtctcg aagaccttca caacagctga
 721 aacaatgtta aatgctcgaa ctcttaagga gtggattgtc tcttctcttg gacctgatgc
 781 tgttgcaaaa catatgattg ctgtcagtac caatcttgag cttgtggaga agtttggaat
 841 tgacccgaaa aatgcttttg cattttggga ctgggttggt ggccgctata gtgtttgcag
 901 tgctgttggt gtcctgccct tatctcttca gtatggcttt ccgattgttc agaaattttt
 961 ggagggtgca gccagcatcg acaaacactt tcgttcatct tcatttgaga aaaatattcc
1021 tgtactcctt ggtttgctga gtgtgtggaa tgtttcattt ctcggatatc cagctagagc
1081 aatattgccc tattcccagg cacttgagaa atttgcacca catattcagc agcttagcat
1141 ggagagtaat ggaaagggtg tctctattga tggcgttcaa ttgtcctttg agactggtga
1201 aattgatttt ggtgaacctg gaaccaatgg gcaacacagc ttctatcaat taatccatca
1261 gggaagagtt attccttgtg attttatcgg tgtcgtaaaa agccagcaac ctgtttactt
1321 gaaaggggaa attgtgagca atcatgacga attgatgtcc aatttctttg ctcagcctga
1381 tgcgcttgct tatggaaaga ctcctgaaca actgcatagc gagaaagtac ctgaacatct
1441 tatccctcat aagacttttc agggcaaccg accatcgctt agtttattgc tgccctcatt
1501 atctgcttat gagattggac agctttttagc catctacgag caccggattg cagtccaggg
1561 tttcctatgg ggaataaact catttgacca gtggggagtg gaactgggca agtctcttgc
1621 ctctcaagtg agaaaatctc tacatgcatc ccgcgttgaa ggaaagcctg tcctgggggtt
1681 taacagcagt actacaagtt tgctgacacg atatcttgct gttgagccat ccactcctta
1741 caacactacc acactgccga aagtttgaca cgacacgttt ggcacgctat tgtcttgagt
1801 taaacaagat tactagagtc ttcatatctt gtaataagtt taagttcgtt ttggagttgt
1861 tacaggctta cagccagttc tacagtactg tagtttcgtt gttttccttt actccgacct
1921 ccaggaaacg aaatggaaaa gaaaaaaaaa ggaaactgtt gttgaataaa taaatcaagt
1981 cgtgtcagca tgaggaagct gtcattaaat aaattaggtg aaaccccgcg cattgctgcg
2041 agaatttagt atgaagatat acattaaaac attatgtaaa ttatgttgga tgataattta
2101 atatgtttgt gtttg
```
//

Revised: October 24, 2001.

May 24 2002 12:27:16

NCBI   **Nucleotide**

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ Go Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save Text   Add to Clipboard

___1: AI726948. BNLGHi6903 Six-da...[gi:5045800]   Taxonomy

IDENTIFIERS

dbEST Id:	2636197
EST name:	BNLGHi6903
GenBank Acc:	AI726948
GenBank gi:	5045800

CLONE INFO

| Clone Id: | (5') |
| DNA type: | cDNA |

PRIMERS

| Sequencing: | T3 Primer |
| PolyA Tail: | Unknown |

SEQUENCE

```
CTTCGGTTCTTCACTTTCCCAGTCTCCAGCAATGGGAGAAACCGATTCTTTCTTCTCGAA
CAAATCAGCGAAGATCTTCGTANCAGGCCATCGAGGCCTAGTTGGTTCTGCCATANTTCG
TAAACTTCAGTCCCTAGGCTTTACCAACCTCCTACTCCGCACCCATGCCGATCTGGACCT
TACTCGCCAATCCGACGTCGAATCCTTCTTCGCCGATGAGAAACCTCACTACGTCGTACT
AGCTGCCGCTAAAGTTGGTGGGATCCACGCCAACAACACTTACCCTGCCGATTTCATTGC
CATCAACCTCCAAATCCAGACCAACGTCATCGATTCCTCTTACCGCCACGGCGTTAACAA
AATCCTCTTCCTCGGTTCCTCTTGTATTTATCCCAAGTTTGCGCCGCAACCCATCCCTGA
AAATGCGCTCTTATCCGGTCCCCTGGAACCCACCAACGAATGGTATGCCGTTGCCAAGAT
CGCGGGGATCAAAATGTGCCAAGCGTACAGAATTCAGCACGGCTTCGATGCTATTTCCGC
TATGCCGACAAATTTGTACGGCCCCAACGATAATTTCCATCCTGAAAATTCCCACGTTTT
GCCCGCTTTGATGCGGAGGTTCCTAAAGCCAAAGTGGATAGAGCAAAAAAAGTAGTTGTG
TGGG
```

| Entry Created: | Jun 11 1999 |
| Last Updated: | Jun 11 1999 |

PUTATIVE ID   Assigned by submitter
                     (AF045286) GDP-4-keto-6-deoxy-D-mannose-3
                     ,5-epimerase-4-reductase [Arabidopsis thaliana]

LIBRARY

Lib Name:	Six-day Cotton fiber
Organism:	Gossypium hirsutum
Cultivar:	Acala Maxxa
Tissue type:	immature fiber
Develop. stage:	Six days post anthesis
Lab host:	XL1-Blue
Vector:	pBluescript II KS+

SUBMITTER

Name:	Ben Burr
Lab:	Biology Department
Institution:	Brookhaven National Laboratory
Address:	Upton, NY 11973, USA
Tel:	516-344-3396

```
Fax:                516-344-3407
E-mail:             burr@bnlux1.bnl.gov
```

CITATIONS
```
Title:              ESTs from developing cotton fiber
Authors:            Blewitt,M., Matz,E.C., Davy,D.F., Burr,B.
Year:               1999
Status:             Unpublished
```

MAP DATA

Revised: October 24, 2001.

May 24 2002 12:14:27

NCBI

Nucleotide

PubMed   Nucleotide   Protein   Genome   Structure   PopSet   Taxonomy   OMIM   Books

Search Nucleotide ▼ for .... Go Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save Text   Add to Clipboard

1: AF045286. Arabidopsis thali...[gi:7596994]   Related Sequences, Protein, PubMed, Taxonomy, LinkOut

```
LOCUS       AF045286                939 bp    DNA     linear   PLN 19-APR-2000
DEFINITION  Arabidopsis thaliana
            GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1) gene,
            complete cds.
ACCESSION   AF045286
VERSION     AF045286.3  GI:7596994
KEYWORDS    .
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Bonin,C.P. and Reiter,W.D.
  TITLE     A bifunctional epimerase-reductase acts downstream of the MUR1 gene
            product and completes the de novo synthesis of GDP-L-fucose in
            Arabidopsis
  JOURNAL   Plant J. 21 (5), 445-454 (2000)
  MEDLINE   20223138
   PUBMED   10758496
REFERENCE   2  (bases 1 to 936)
  AUTHORS   Bonin,C.P., Potter,I., Vanzin,G.F. and Reiter,W.-D.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JAN-1998) Molecular and Cell Biology, University of
            Connecticut, 75 North Eagleville Road, Storrs, CT 06269, USA
REFERENCE   3  (bases 1 to 936)
  AUTHORS   Bonin,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-1999) Molecular and Cell Biology, University of
            Connecticut, 75 North Eagleville Road, Storrs, CT 06269, USA
  REMARK    Sequence update by submitter
REFERENCE   4  (bases 1 to 939)
  AUTHORS   Reiter,W.-D.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Molecular and Cell Biology, University of
            Connecticut, 75 North Eagleville Road, Storrs, CT 06269, USA
  REMARK    Sequence update by submitter
COMMENT     On Apr 19, 2000 this sequence version replaced gi:6016478.
FEATURES             Location/Qualifiers
     source          1..939
                     /organism="Arabidopsis thaliana"
                     /cultivar="Columbia ecotype"
                     /db_xref="taxon:3702"
     gene            <1..>939
                     /gene="GER1"
     mRNA            <1..>939
                     /gene="GER1"
                     /product="GDP-4-keto-6-deoxy-D-mannose-3,
                     5-epimerase-4-reductase"
     CDS             1..939
                     /gene="GER1"
                     /note="enzyme in pathway for de novo synthesis of
```

```
                GDP-L-fucose"
                /codon_start=1
                /product="GDP-4-keto-6-deoxy-D-mannose-3,
                5-epimerase-4-reductase"
                /protein_id="AAC02703.2"
                /db_xref="GI:6016479"
                /translation="MSDKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLT
                RQADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVK
                KLLFLGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDA
                ISGMPTNLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDD
                LADACVFLLDRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRK
                LMDSSKLASLGWTPKVSLRDGLSQTYDWYLKNVCNR"
BASE COUNT       229 a      190 c      240 g      280 t
ORIGIN
        1 atgtctgaca aatctgccaa aatcttcgtc gcgggtcatc gtggtttggt tggatctgcc
       61 attgtccgca agcttcagga acaaggtttc accaatctcg ttcttaaaac acacgccgag
      121 cttgatctca ctcgtcaagc cgatgttgaa tccttctttt ctcaagagaa gccagtttat
      181 gtaatcctag cagcagctaa agttggtggt attcacgcta acaacaccta tcctgctgat
      241 ttcattggtg tcaatctcca gattcagacc aatgtgatcc actctgcata tgagcacggt
      301 gtgaagaagc ttctcttcct tggatcatcc tgcatttacc ctaaatttgc tcctcagcca
      361 attcctgagt ctgctttgtt aacagcatcg cttgaaccaa ctaatgagtg gtatgctatt
      421 gctaagatcg ctgggattaa gacttgtcag gcttatagga ttcagcacgg atgggatgca
      481 atctctggca tgcctactaa tctctatggt cctaatgaca atttccaccc ggagaattct
      541 catgtgcttc ctgctcttat gaggaggttc cacgaggcga aagtgaatgg agcggaggaa
      601 gttgtggtgt ggggtacagg tagtccgttg agggagttct tgcatgttga tgatttggct
      661 gatgcttgtg ttttcttgct ggatcgatac agcgggttgg agcatgttaa cattggaagt
      721 ggtcaagaag tgactattag agagttggct gagttggtga aagaggttgt tggtttttgaa
      781 gggaagcttg atgggattg cactaagcca gatggcacac cgaggaaact tatggacagc
      841 tcaaagctcg cgtctttggg ttggacacct aaggtttctc ttagagatgg tctgagccaa
      901 acttatgatt ggtatttgaa gaatgtttgc aaccgataa
//
```

Revised: October 24, 2001.

May 24 2002 12:27:16

NCBI

Nucleotide

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ | Go | Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ | Save | Text | Add to Clipboard

1: AF076484. Arabidopsis thali...[gi:3598957]   Related Sequences, Protein, Taxonomy, LinkOut

```
LOCUS       AF076484                1490 bp    mRNA    linear   PLN 20-NOV-1998
DEFINITION  Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA,
            complete cds.
ACCESSION   AF076484
VERSION     AF076484.1  GI:3598957
KEYWORDS    .
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1490)
  AUTHORS   Weers,B. and Thornburg,R.
  TITLE     Characterization of the cDNA and Gene for the Arabidopsis thaliana
            GDP-Mannose Pyrophosphorylase (Accession No. AF076484). (PGR98-175)
  JOURNAL   Plant Physiol. 118 (3), 1101 (1998)
REFERENCE   2  (bases 1 to 1490)
  AUTHORS   Weers,B. and Thornburg,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-1998) Biochemistry and Biophysics, Iowa State
            University, Ames, IA 50011, USA
FEATURES             Location/Qualifiers
     source          1..1490
                     /organism="Arabidopsis thaliana"
                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="II"
                     /map="near 72 cM"
                     /clone="Arabidopsis Biological Resource Center number
                     132P5T7"
                     /clone_lib="Lambda PRL2 derived from equal quantities of
                     four pools of mRNA:  7 day germinated etiolated seedlings;
                     tissue culture grown roots; rosettes from staged plants
                     half with 24 hour light cycle, half with 16 hr light, 8
                     hour dark cycle; aerial tissue (stems, flowers and
                     siliques) from staged plants half with 24 hour light
                     cycle, half with 16 hr light, 8 hour dark cycle"
     gene            1..1490
                     /gene="GMP1"
     misc_feature    1..1490
                     /gene="GMP1"
                     /note="similar to genomic sequence deposited in GenBank
                     Accession Number AC003000"
     CDS             153..1238
                     /gene="GMP1"
                     /function="vitamin C biosynthesis"
                     /function="glycoprotein biosynthesis"
                     /note="GTP mannose-1-phosphate guanylyltransferase"
                     /codon_start=1
                     /product="GDP-mannose pyrophosphorylase"
                     /protein_id="AAC78474.1"
                     /db_xref="GI:3598958"
```

```
                    /translation="MKALILVGGFGTRLRPLTLSFPKPLVDFANKPMILHQIEALKAV
                    GVDEVVLAINYQPEVMLNFLKDFETKLEIKITCSQETEPLGTAGPLALARDKLLDGSG
                    EPFFVLNSDVISEYPLKEMLEFHKSHGGEASIMVTKVDEPSKYGVVVMEESTGRVEKF
                    VEKPKLYVGNKINAGIYLLNPSVLDKIELRPTSIEKETFPKIAAAQGLYAMVLPGFWM
                    DIGQPRDYITGLRLYLDSLRKKSPAKLTSGPHIVGNVLVDETATIGEGCLIGPDVAIG
                    PGCIVESGVRLSRCTVMRGVRIKKHACISSSIIGWHSTVGQWARIENMTILGEDVHVS
                    DEIYSNGGVVLPHKEIKSNILKPEIVM"
     polyA signal   1457..1463
                    /gene="GMP1"
     polyA site     1475
                    /gene="GMP1"
BASE COUNT        412 a      290 c      345 g      443 t
ORIGIN
        1 cgttttgcca acgaacgttc tttcttctta atcacagctc agcctgacgc aaccgctcag
       61 gctgatctct tccaatttac aggcatttcc cagctcaaat ctctgatccg gtgagatctc
      121 tctcaaggaa aaggagttag agcatcatca agatgaaggc actcattctt gttggaggct
      181 tcggcactcg cttgagacca ttgactctca gtttcccaaa gccccttgtt gattttgcta
      241 ataaacccat gatccttcat cagatagagg ctcttaaggc agttggagtt gatgaagtgg
      301 ttttggccat caattatcag ccagaggtga tgctgaactt cttgaaggac tttgagacca
      361 agctggaaat caaaatcact tgctcacaag agaccgagcc actaggtacc gctggtcctc
      421 tggctctagc gagagacaaa ttgcttgatg gatctggaga gcccttcttt gttcttaaca
      481 gtgatgtgat tagtgagtac cctcttaaag aaatgcttga gtttcacaaa tctcacggtg
      541 gggaagcctc cataatggta acaaaggtgg atgaaccgtc gaaatatgga gtggttgtta
      601 tggaagaaag cactggaaga gtggagaagt ttgtggaaaa gccaaaactg tatgtaggta
      661 acaagatcaa cgctgggatt tatcttctga acccatctgt tcttgataag attgagctaa
      721 gaccgacttc aatcgaaaaa gagactttcc ctaagattgc agcagcgcaa gggctctatg
      781 ctatggtgct accagggttt tggatggaca ttgggcaacc ccgtgactac ataacggggtt
      841 tgagactcta cttagactcc cttaggaaga aatctcctgc caaattaacc agtgggccac
      901 acatagttgg gaatgttctt gttgacgaaa ccgctacaat tggggaagga tgtttgattg
      961 gaccagacgt tgccattggt ccaggctgca ttgttgagtc aggagtcaga ctctcccgat
     1021 gcacggtcat gcgtggagtc cgcatcaaga agcatgcgtg tatctcgagc agtatcatcg
     1081 ggtggcactc aacggttggt caatgggcca ggatcgagaa catgacgatc ctcggtgagg
     1141 atgttcatgt gagcgatgag atctatagca atggaggagt tgttttgcca cacaaggaga
     1201 tcaaatcaaa catcttgaag ccagagatag tgatgtgaaa atgagatatt atatgtgcaa
     1261 ctttttttt tttttgtgt cctttcttca actttgaaat cgctttcgta attcttaatg
     1321 gcttttgaat aagcatcaat caaaacgctg tatatcttgt tagggtcgtt tgctgttttg
     1381 tctctttttt tgttttgtaa tttataaaaa aatttattct cattttatgt gagatacttt
     1441 tgaatattca ttaattataa agcttttttt ttgtgaaaaa aaaaaaaaa
//
```

Revised: October 24, 2001.

May 24 2002 12:27:16

NCBI

Nucleotide

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ Go Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save Text | Add to Clipboard

1: AF022716. Solanum tuberosum...[gi:4103323]   Protein, Taxonomy

```
LOCUS       AF022716                1478 bp    mRNA    linear   PLN 05-JAN-1999
DEFINITION  Solanum tuberosum GDP-mannose pyrophosphorylase (Gmp) mRNA,
            complete cds.
ACCESSION   AF022716
VERSION     AF022716.1  GI:4103323
KEYWORDS    .
SOURCE      potato.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 1478)
  AUTHORS   Keller,R., Kossmann,J. and Willmitzer,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1997) MPI fuer Molekulare Pflanzenphysiologie,
            Karl-Liebknecht-Str. 25, Haus 20, Golm 14476, Germany
FEATURES             Location/Qualifiers
     source          1..1478
                     /organism="Solanum tuberosum"
                     /db_xref="taxon:4113"
     gene            1..1478
                     /gene="Gmp"
     CDS             136..1221
                     /gene="Gmp"
                     /codon_start=1
                     /product="GDP-mannose pyrophosphorylase"
                     /protein_id="AAD01737.1"
                     /db_xref="GI:4103324"
                     /translation="MKALILVGGFGTRLRPLTLSVPKPLVEFANKPMILHQIEALKAV
                     GVTEVVLAINYQPEVMLNFLKEFEASLGIKITCSQETEPLGTAGPLALARDKLIDDSG
                     EPFFVLNSDVISEYPFKEMIQFHKSHGGEASLMVTKVDEPSKYGVVVMEESTGQVERF
                     VEKPKLFVGNKINAGFYLLNPSVLDRIQLRPTSIEKEVFPKIAAEKKLYAMVLPGFWM
                     DIGQPRDYITGLRLYLDSLKKHSSPKLASGPHIVGNVIVDESAKIGEGCLIGPDVAIG
                     SGCVIESGVRLSRCTVMRGVRIKKHACISGSIIGWHSTVGQWARVENMTILGEDVHVC
                     DEIYSNGGVVLPHKEIKSSILKPEIVM"
BASE COUNT      395 a     279 c     334 g     470 t
ORIGIN
        1 ctaaacacac tcactcccct tcttctttct tgtttgttcg gttgggtctc tctctgactt
       61 gagtccactc attcttcaat tcagtctttg gattttctcg atctacaatt cttaaaggaa
      121 ctttgatatc tcaagatgaa ggcacttatc cttgttggag ggttcggtac tcggctcagg
      181 ccactcaccc tcagtgtccc aaagccactc gtcgaatttg ctaacaaacc aatgatttg
      241 catcagattg aggctctcaa ggctgttgga gtaaccgaag ttgtactggc tattaactac
      301 caacctgagg tgatgctgaa cttcttgaaa gaatttgagg caagccttgg aatcaagatc
      361 acctgttctc aagaaactga accacttggc actgctggtc cccttgcttt ggctagagat
      421 aagctgatag atgactctgg tgaaccattt tttgttctta acagtgatgt tatcagtgaa
      481 tatccattca aggagatgat tcaattccac aaatcccatg gtggtgaggc ttctttgatg
      541 gtgaccaagg tggatgagcc ttctaaatat ggtgttgttg tcatggaaga atccactggg
      601 caagtagaga gatttgtgga gaagccaaag ttatttgttg gcaacaagat caatgctgga
      661 ttttacctgc tgaacccttc tgtcctagac agaattcaat tacggccaac atcaattgag
      721 aaagaggttt ttccaaaaat tgcagcagag aagaaactgt atgcaatggt gctacctgga
      781 ttttggatgg acattggcca accaagagat tacattactg gcctcagact ctatctggat
      841 tctttaaaga aacactcttc acctaaattg gcttcaggac cacacattgt cggaaatgtc
```

```
 901 atagtggatg aatctgccaa gattggagag ggttgtttga taggaccaga tgttgcaatt
 961 ggttctggtt gtgtgattga gtctggagtt agactctccc gttgcactgt gatgcgagga
1021 gtccgcatca agaaacatgc atgcatctca ggtagcatca ttggctggca ctctactgtt
1081 ggacaatggg ctcgtgttga gaacatgacc attctcgggg aagatgtcca tgtttgtgat
1141 gaaatttaca gcaatggagg tgtagttttg ccccacaagg agatcaaatc cagtatattg
1201 aaacctgaaa tcgtgatgtg aggatatgct tgttagcact aggaaaaata taagtttatg
1261 tattcagttc tttatgatgt cttttttcctt acctattcct gatttggttg gtttccagtt
1321 ctcttcttct tcaagtgtga aaagtcggtc ctgagaattc gagtgatgta aacttttctt
1381 gctgaattgt tgttatgttg tgaaaggtat gagatattgt aagactggga aatgtgtaat
1441 ttttgttata tatagataaa taaagtttcc ccttaaaa
//
```

Revised: October 24, 2001.

May 24 2002 12:27:16

NCBI   **Nucleotide**

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Books |

Search Nucleotide ▼ for _____ Go Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save Text   Add to Clipboard

1: AI726749. BNLGHi6495 Six-da...[gi:5045601]   Taxonomy

IDENTIFIERS

dbEST Id:	**2635998**
EST name:	BNLGHi6495
GenBank Acc:	AI726749
GenBank gi:	5045601

CLONE INFO
Clone Id:	(5')
DNA type:	cDNA

PRIMERS
Sequencing:	T3 Primer
PolyA Tail:	Unknown

SEQUENCE

```
ACCAGATCTCATCCCCCCAACACATTATTTAGTCCCCCCTAAGTTCCGCCATTAAAGCTC
TTCATTAACTTCATTCCCTTTGCTTATTTTCTATTACAATTACAGCCCATTTTTCTAAAC
TCCATCAATATTCAAAAAGGAACTTCAATGGCTCTAAAGAAATCTGGTTTGATTGCTTTA
TTTGATGTTGATGGAACACTTACAGCTCCAAGAAAGGTGGCTACCCCTGAAATGCTGGAG
TTCATGAAGGAACTGAGAAAGGTTGTTACTGTTGGAGTAGTACGTGGATCTGATCTTGTT
AACATATCTGAGCAACTTGGGAAATCANTGATTAATGACTATGATTATGTATTTTCTGAA
AATGGACTTGTTGCTCATAAAGATGGGAAACTCATTGGAACCCAGAGTTTGAAGTCGTTT
CTCGGAGAAGATAAGCTGAAGGAATTTATAAACTTCACATTGCATTATATTGCTGACTTG
GATATCTCGATAAAAAGGGGGACATTCATTGAATTCCGAAGTGGGATGCTTAATGTATCT
CCGATTGGACGTAACTGGTACCCAGAAGAAGAGGATGAATTCCAANAGTACGACGAGGTT
CACAATATTCCCCTGAAAATGGTGTCTGTACTTCGAGAAAAGTTTGCTCACCTTTAACTT
GACATTTTTCAATG
```

Entry Created:	Jun 11 1999
Last Updated:	Jun 11 1999

PUTATIVE ID	Assigned by submitter
	(AC004665) putative phosphomannomutase [Arabidopsis thaliana]

LIBRARY
Lib Name:	Six-day Cotton fiber
Organism:	Gossypium hirsutum
Cultivar:	Acala Maxxa
Tissue type:	immature fiber
Develop. stage:	Six days post anthesis
Lab host:	XL1-Blue
Vector:	pBluescript II KS+

SUBMITTER
Name:	Ben Burr
Lab:	Biology Department
Institution:	Brookhaven National Laboratory
Address:	Upton, NY 11973, USA
Tel:	516-344-3396

```
Fax:              516-344-3407
E-mail:           burr@bnlux1.bnl.gov
```

CITATIONS
```
Title:            ESTs from developing cotton fiber
Authors:          Blewitt,M., Matz,E.C., Davy,D.F., Burr,B.
Year:             1999
Status:           Unpublished
```

MAP DATA

Revised: October 24, 2001.

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 24 2002 12:14:27

NCBI **Nucleotide**

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books

Search Nucleotide ▼ for _____ Go Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Save Text   Add to Clipboard

1: AC004665. Arabidopsis thali...[gi:20197203]   Related Sequences, Protein, Taxonomy, LinkOut

```
LOCUS       AC004665              101647 bp    DNA     linear   PLN 11-MAR-2002
DEFINITION  Arabidopsis thaliana chromosome 2 clone F4I18 map CIC02E07,
            complete sequence.
ACCESSION   AC004665
VERSION     AC004665.3  GI:20197203
KEYWORDS    HTG.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 101647)
  AUTHORS   Rounsley,S.D., Lin,X., Ketchum,K.A., Crosby,M.L., Brandon,R.C.,
            Sykes,S.M., Kaul,S., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
            Somerville,C.R. and Venter,J.C.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 101647)
  AUTHORS   Lin,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA
REFERENCE   3  (bases 1 to 101647)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT     On Apr 18, 2002 this sequence version replaced gi:6598428.
FEATURES             Location/Qualifiers
     source          1..101647
                     /organism="Arabidopsis thaliana"
                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="2"
                     /map="CIC02E07"
                     /clone="F4I18"
     misc_feature    1..13498
                     /note="overlap with BAC clone T3F17
                     (AC005397:96652..110149)."
     gene            complement(150..3568)
                     /gene="At2g46010"
                     /note="F4I18.1; predicted by genscan and genefinder"
     mRNA            complement(join(<150..266,437..1744,1868..3142,
                     3440..>3568))
                     /gene="At2g46010"
     CDS             complement(join(150..266,437..1744,1868..3142,3440..3568))
                     /gene="At2g46010"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="AAM14971.1"
                     /db_xref="GI:20197206"
                     /translation="MGPAGRTASTSSAASPSSSSSSVQQQQQQQQQQQQQQQLASRQQ
                     QQQHRNSDTNENMFAYQPGGVQGMMGGGNFASSPGSMQMPQQSRNFFESPQQQQQQQQ
```